

## AMENDMENTS TO THE SPECIFICATION:

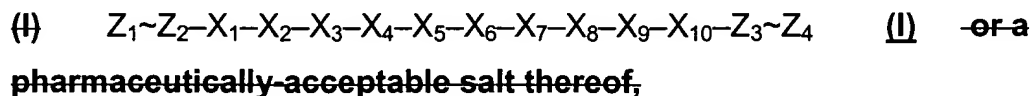
Please amend the following passage of the specification appearing on p. 57, ln. 20-29:

Such formats include, but are not limited to, Protein Data Bank ("PDB") format (Research Collaboratory for Structural Bioinformatics; ~~http://www.rcsb.org/pdb/docs/format/pdbguide2.2/guide2.2\_frame.html~~); Cambridge Crystallographic Data Centre format (~~http://www.ccdc.cam.ac.uk/support/csd\_doc/volume3/z323.html~~); Structure-data ("SD") file format (MDL Information Systems, Inc.; Dalby et al., 1992, J. Chem. Inf. Comp. Sci. 32:244-255), and line-notation, e.g., as used in SMILES (Weininger, 1988, J. Chem. Inf. Comp. Sci. 28:31-36). Methods of converting between various formats read by different computer software will be readily apparent to those of skill in the art, e.g., BABEL (v. 1.06, Walters & Stahl, ©1992, 1993, 1994; ~~http://www.brunel.ac.uk/departments/chem/babel.htm~~.)

## AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claim 1 (currently amended): An isolated compound which inhibits pilus assembly, or a pharmaceutically-acceptable salt thereof, said compound comprising a mimic of a chaperone G1 beta-strand or a mimic of an amino terminal motif of a pilus subunit, wherein the mimic is a 10 to 20 residue peptide, having an amino terminus and a carboxy terminus, according to formula (I):



wherein:

$Z_1$  is the amino terminus of the mimic peptide,  $Z_1$  having the formula R-C(O)-NR- or RRN-;

$Z_2$  is (i) a first peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting  $Z_1$  to  $X_1$ ;